

In the Specification:

Please amend the specification as follows:

On page one of the specification, please delete lines 9-14 following the phrase "CROSS-REFERENCE TO RELATED APPLICATIONS" on line 8 and insert the following paragraph in place thereof:

-- The present application is a divisional of U.S. Application No. 09/579,536, filed May 24, 2000, which is a continuation-in-part of U.S. Application No. 09/199,865, filed on November 25, 1998, which is a continuation of PCT Application No. PCT/US97/09407 US/PCT97/09407, filed on May 30, 1997, all of which are entitled to priority under 35 U.S.C. § 119(e), to U.S. Provisional Application No. 60/018,841, filed on May 31, 1996, and all of which are hereby incorporated herein by reference in their entirety. --

Please replace the paragraph beginning at line 5 and extending to line 8 on page 5 of the specification with the following paragraph:

-- Carboxy terminal to this region is a polyglutamine-rich domain (OPA) and a pro-glu-ser-thr (PEST) domain (SEQ ID NO:33) which may be involved in signaling protein degradation. There are numerous Notch homologs, including three Notch genes. (The corresponding structures for Lin-12 and Glp-1 are shown in Figure 4.) --

Please replace the paragraph beginning at line 29 on page 24 and extending to line 15 on page 25 of the specification with the following paragraph:

-- The determination of percent identity between two nucleotide or amino acid sequences can be accomplished using a mathematical algorithm. For example, a mathematical algorithm useful for comparing two sequences is the algorithm of Karlin and Altschul (1990, Proc. Natl. Acad. Sci. USA 87:2264-2268), modified as in Karlin and Altschul (1993, Proc. Natl. Acad. Sci. USA 90:5873-5877). This algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990, J. Mol. Biol. 215:403-410), and can be accessed, for example,

at the National Center for Biotechnology Information (NCBI) world wide web site having the universal resource locator "<http://www.ncbi.nlm.nih.gov/BLAST/>". BLAST nucleotide searches can be performed with the NBLAST program (designated "blastn" at the NCBI web site), using the following parameters: gap penalty = 5; gap extension penalty = 2; mismatch penalty = 3; match reward = 1; expectation value 10.0; and word size = 11 to obtain nucleotide sequences homologous to a nucleic acid described herein. BLAST protein searches can be performed with the XBLAST program (designated "blastn" at the NCBI web site) or the NCBI "blastp" program, using the following parameters: expectation value 10.0, BLOSUM62 scoring matrix to obtain amino acid sequences homologous to a protein molecule described herein. --

Please replace the paragraph beginning at line 16 and extending to line 22 on page 25 of the specification with the following paragraph:

-- To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997, Nucleic Acids Res. 25:3389-3402). Alternatively, PSI-Blast or PHI-Blast can be used to perform an iterated search which detects distant relationships between molecules (*id.*) and relationships between molecules which share a common pattern. When utilizing BLAST, Gapped BLAST, PSI-Blast, and PHI-Blast programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov> National Center for Biotechnology Information world wide web site. --

Please replace the paragraph beginning at line 10 and extending to line 14 on page 128 of the specification with the following paragraph:

-- Analysis of differential gene expression by SAGE also demonstrated that the soluble Jagged-1 transfectants were able to differentially express 227 transcripts of comprising either known or novel sequences. These results were posted at URL <http://Zappa.mmeri.mmc.org/~varye/jag> the web site for the Maine Medical Center Research Institute, and a selected number are listed in Table 1. --

On page 128, at line 16, please delete Table 1, and kindly insert the following
Table 1 in place thereof:

TABLE 1
Most Frequently Observed SAGE Tags

RNA Source	Tags Sequenced	Discrete Tags	mRNA Species
Insert-less Vector	1428	982	197
Soluble Jagged-1	3150	1647	336
Totals	4578	2629	533

Tag Count SEQ Acc. No. Description
 ID NO:

Tags Predominant in Soluble Jagged-1 NIH 3T3 Cell Transfectants

TGGATCAGTC	14	<u>34</u>	M62952	<i>Mus musculus</i> ribosomal protein L19
TAAAGAGGCC	9	<u>35</u>	U67770	<i>Mus musculus</i> ribosomal protein S26 (RPS26) mRNA
CCTGATCTT	8	<u>36</u>	X06406	Mouse mRNA for translational controlled 40 kDa protein
TGTAACAGGA	8	<u>37</u>	X04648	Mouse mRNA for IgG1/IgG2b Fc receptor (FcR)
TCTGTGCACC	6	<u>38</u>	U93864	<i>Mus musculus</i> ribosomal protein S11 mRNA
CCAAATAAAA	6	<u>39</u>	U13687	<i>Mus musculus</i> DBA/2J lactate dehydrogenase-A
CTAATAAAAG	6	<u>40</u>	X54691	Mouse COX4 MrnA for cytochrome c oxidase subunit
GCCAAGGGTC	6	<u>41</u>	L08651	<i>Mus musculus</i> large ribosomal subunit protein mRNA
GTCTGCTGAT	5	<u>42</u>	X75313	M. musculus (C57BL/6) GB-like mRNA
AAGGAAGAGA	4	<u>43</u>	X51438	Mouse mRNA for vimentin
TGAAATAAAC	4	<u>44</u>	M33212	Mouse nucleolar protein N038 mRNA
CACCACCACA	4	<u>45</u>	X05021	Murine mRNA with homology to yeast L29 ribosomal prot.
CCTCAGCCTG	4	<u>46</u>	X52886	<i>Mus musculus</i> mRNA for cathepsin D.
CTCTGACTTA	4	<u>47</u>	Y16256	<i>Mus musculus</i> mRNA for basigin
GTGGGCGTGT	4	<u>48</u>	M33330	Mouse insuloma (rig)mRNA
TCCTTGGGGG	4	<u>49</u>	U60001	<i>Mus musculus</i> protein kinase C inhibitor (mPKCI) mRNA

Tags Predominant in Control Insert-less Vector NIH 3T3 Cell Tranfectants

CGCCTGCTAG	3	<u>50</u>	X58251	Mouse COL1A2 mRNA for pro-alpha-2(I) collagen
AAAAAAAAAAA	2	<u>51</u>	AF0253	<i>Mus musculus</i> tssk-1 and tssk-2 kinase substrate mRNA
AAGCAGAAGG	2	<u>52</u>	M16465	Mouse calpactin I light chain (p11) mRNA complete
CAGGACTCCG	2	<u>53</u>	M26270	Mouse stearoyl-CoA desaturase (SCD2) mRNA
GAAGCAGGAC	2	<u>54</u>	D00472	Mouse mRNA for cofilin
GGATATGTGG	2	<u>55</u>	M20157	Mouse Egr-1 mRNA
GTTCTGATTG	2	<u>56</u>	U88588	<i>Mus musculus</i> cdr2 mRNA